



#7

SEQUENCE LISTING

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Rohlf, Christian

<120> DPI-6, A PUTATIVE THERAPEUTIC TARGET AND BIOMARKER IN NEUROPSYCHIATRIC AND NEUROLOGICAL DISORDERS

<130> 2543-1-008/PCT US

<140> US 10/051,618
<141> 2001-10-24

<150> GB 0004412.3
<151> 2000-02-24

<150> GB 0004415.6
<151> 2000-02-24

<150> GB 0006285.2
<151> 2000-03-15

<150> GB 0028734.2
<151> 2000-11-24

<150> US 09/724,391
<151> 2000-11-28

<150> US 09/750,395
<151> 2000-11-28

<150> GB 0030050.9
<151> 2000-12-08

<150> US 60/254,830
<151> 2000-12-12

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<170> PatentIn version 3.0

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Thr Leu Leu Cys Leu Leu Ala Ala Val Pro Thr Ala Pro Ala			
10	15	20	
ccc gct ccg acg gcg acc tcg gct cca gtc aag ccc ggc ccg gct ctc			151
Pro Ala Pro Thr Ala Thr Ser Ala Pro Val Lys Pro Gly Pro Ala Leu			
25	30	35	
agc tac ccg cag gag gag gcc acc ctc aat gag atg ttc cgc gag gtt			199
Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe Arg Glu Val			
40	45	50	
gag gaa ctg atg gag gac acg cag cac aaa ttg cgc agc gcg gtg gaa			247
Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser Ala Val Glu			
55	60	65	70
gag atg gag gca gaa gaa gct gct aaa gca tca tca gaa gtg aac			295
Glu Met Glu Ala Glu Glu Ala Ala Lys Ala Ser Ser Glu Val Asn			
75	80	85	
ctg gca aac tta cct ccc agc tat cac aat gag acc aac aca gac acg			343
Leu Ala Asn Leu Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr			
90	95	100	
aag gtt gga aat aat acc atc cat gtg cac cga gaa att cac aag ata			391
Lys Val Gly Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile			
105	110	115	
acc aac aac cag act gga caa atg gtc ttt tca gag aca gtt atc aca			439
Thr Asn Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr			
120	125	130	
tct gtg gga gac gaa gaa ggc aga agg agc cac gag tgc atc atc gac			487
Ser Val Gly Asp Glu Glu Gly Arg Arg Ser His Glu Cys Ile Ile Asp			
135	140	145	150
gag gac tgt ggg ccc agc atg tac tgc cag ttt gcc agc ttc cag tac			535
Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln Phe Ala Ser Phe Gln Tyr			
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acc tgc cag cca tgc cgg ggc cag agg atg ctc tgc acc cgg gac agt			583
Thr Cys Gln Pro Cys Arg Gly Gln Arg Met Leu Cys Thr Arg Asp Ser			
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gag tgc tgt gga gac cag ctg tgt gtc tgg ggt cac tgc acc aaa atg			631
Glu Cys Cys Gly Asp Gln Leu Cys Val Trp Gly His Cys Thr Lys Met			
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gcc acc agg ggc agc aat ggg acc atc tgt gac aac cag agg gac tgc			679
Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys Asp Asn Gln Arg Asp Cys			
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cag ccg ggg ctg tgc tgt gcc ttc cag aga ggc ctg ctg ttc cct gtg Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu Phe Pro Val 215	220	225	230	727
tgc aca ccc ctg ccc gtg gag ggc gag ctt tgc cat gac ccc gcc agc Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp Pro Ala Ser 235	240	245		775
cg g ctt ctg gac ctc atc acc tgg gag cta gag cct gat gga gcc ttg Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Ala Leu 250	255	260		823
gac cga tgc cct tgt gcc agt ggc ctc ctc tgc cag ccc cac agc cac Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro His Ser His 265	270	275		871
agc ctg gtg tat gtg tgc aag ccg acc ttc gtg ggg agc cgt gac caa Ser Leu Val Tyr Val Cys Lys Pro Thr Phe Val Gly Ser Arg Asp Gln 280	285	290		919
gat ggg gag atc ctg ctg ccc aga gag gtc ccc gat gag tat gaa gtt Asp Gly Glu Ile Leu Leu Pro Arg Glu Val Pro Asp Glu Tyr Glu Val 295	300	305	310	967
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agc ctg act gaa gag atg gcg ctg ggg gag cct gcg gct gcc gct Ser Leu Thr Glu Glu Met Ala Leu Gly Glu Pro Ala Ala Ala Ala 330	335	340		1063
gca ctg ctg gga ggg gaa gag att tag atctggacca ggctgtgggt Ala Leu Leu Gly Gly Glu Glu Ile 345	350			1110
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Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val		
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Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn		
35	40	45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys		
50	55	60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys			
65	70	75	80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn		
85	90	95

Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His		
100	105	110

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe		
115	120	125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
145 150 155 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
180 185 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
325 330 335

Pro Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile
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